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Nucleotide Sequence of Rhesus Monkey BRS-3

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1  ATGGCTCAAA GGCAGCCTCA CTCACCTAAT CAGACTTTAA TTTCAATCAC
51 AAATGACACA GAATCAAGCT CTGTGGTTTC TAACGATAAC ACAAATAAAG
101 GACGGAGCGG GGACAACTCT CCAGGAATAG AAGCATTGTG TGCCATCTAT
151 ATTACTTATG CTGTGATCAT TTCAGTGGGC ATCCTTGGAA ATGCTATTCT
201 CATCAAAGTC TTTTTCAGA CCAAATCCAT GCAAACAGTT CCAAATATTT
251 TCATCACCAG CCTGGCTTTT GGAGATCTTT TACTTCTGCT AACTTGTGTG
301 CCAGTGGATG CAACCCACTA CCTTGCAGAA GGATGGCTGT TCGGAAGAAT
351 TGGTTGTAAG GTGCTCTCTT TCATCCGGCT CACTTCTGTT GGTGTGTCAG
401 TGTTACGTT AACAATTCTC AGCGCTGACA GATACAAGGC AGTTGTGAAG
451 CCACTTGAGC GACAGCCCTC CAATGCCATC CTGAAGACTT GTATAAAAGC
501 TGGCTGCGTC TGGATCGTGT CTATGATATT TGCTCTACCT GAGGCTATAT
551 TTTCAAATGT ATATTCTTTT CGAGATCCCA ACAAAAATGT GACATTTGAA
601 TCGTGTACCT CTTATCCTGT CTCTAAGAAG CTCTTGCAAG AAATACATTG
651 TCTGCTGTGC TTCTTAGTGT TCTACATTAT TCCACTCTCT ATTATCTCTG
701 TCTATTATTC TTTGATTGCT AGGACCCTTT ATAAAAGCAC CCTGAACATA
751 CCTACTGAGG AACAAGGCCA TGCCCGTAAG CAGATTGAAT CCCGGAAGAG
801 AATTGCCAGA ACGGTATTGG TGTTGGTGGC TCTGTTTGCC CTCTGCTGGT
851 TGCCAAATCA CCTCCTGTAC CTCTACCATT CATTCACTTC TCAAACCTAT
901 GTAGACCCCT CTGCCATGCA TTTCATTTTC ACCATTTTCT CTCGGGTTCT
951 GGCTTTCAGC AATTCTTGCG TAAACCCCTT TGCTCTCTAC TGGCTGAGCA
1001 AAACCTTCCA GAAGCATTTT AAAGCTCAGT TGTTCGTGTG CAAGGCAGAG
1051 CAGCCTGAGC CTCCTGTTGC TGACACCTCT CTTACCACCC TGGCTGTGAT
1101 GGAAGGGTC CCGGGCACTG GGAACATGCA GATGTCTGAA ATTAGTGTGA
1151 CCTCGTTCCC TGGGTGTAGT GTGAAGCAGG CAGAGGATAG AGTCTAG

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FIG.1

(SEQ ID NO:1)

Amino Acid Sequence of Rhesus Monkey BRS-3 Protein

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1  MAQRQPHSPN QTLISITNDT ESSSVVSDN TNKGRSGDNS PGIEALCAIY
51 ITYAVIISVG ILGNAILIKV FFKTKSMQTV PNIFITSLAF GDLLLLLTCV
101 PVDATHYLAE GWLFGRIGCK VLSFIRLTSV GVSVFTLIL SADRYKAVVK
151 PLERQPSNAI LKTCIKAGCV WIVSMIFALP EAIFSNVYSF RDPNKNVTFE
201 SCTSYPVSKK LLQEIHSLLC FLVFIIPLS IISVYYSLIA RTLYKSTLNI
251 PTEEQGHARK QIESRKRIAR TVLVLVALFA LCWLPNHLLY LYHSFTSQTY
301 VDPSAMHFIF TIFSRVLAFS NSCVNPFALY WLSKTFQKHF KAQLFCCKAE
351 QPEPPVADTS LTTLAVMGRV PGTGNMQMSE ISVTSFPGCS VKQAEDRV

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(SEQ ID NO:2)

FIG.2

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ALIGNMENT OF BRS-3 NUCLEOTIDE SEQUENCES

	(1)	1	10	20	30	40	52
hBRS3	(1)	ATGGCTCAAAGGCAGCCTCACTCACCTAATCAGACTTTAATTTCAATCACAA					
ratBRS3	(1)	ATGTCTCAAAGGCAGCCTCAGTCACCTAATCAGACTTTAATTTCCATTACAA					
rhBRS3	(1)	ATGGCTCAAAGGCAGCCTCACTCACCTAATCAGACTTTAATTTCAATCACAA					
Consensus	(1)	ATGGCTCAAAGGCAGCCTCACTCACCTAATCAGACTTTAATTTCAATCACAA					
	(53)	53	60	70	80	90	104
hBRS3	(53)	ATGACACAGAATCATCAAGCTCTGTGGTTTCTAACGATAACACAAATAAAGG					
ratBRS3	(53)	ATGACACAGAAACATCAAGCTCTGCCGTCTCCAACGATACTACACCTAAAGG					
rhBRS3	(53)	ATGACACAGA__ATCAAGCTCTGTGGTTTCTAACGATAACACAAATAAAGG					
Consensus	(53)	ATGACACAGAA CATCAAGCTCTGTGGTTTCTAACGATAACACAAATAAAGG					
	(105)	105	110	120	130	140	156
hBRS3	(105)	ATGGAGCGGGGACAACCTCTCCAGGAATAGAAGCATTGTGTGCCATCTATATT					
ratBRS3	(105)	ATGGACCGGAGACAACCTCTCCAGGAATAGAAGCACTGTGTGCCATCTATATC					
rhBRS3	(102)	ACGGAGCGGGGACAACCTCTCCAGGAATAGAAGCATTGTGTGCCATCTATATT					
Consensus	(105)	ATGGAGCGGGGACAACCTCTCCAGGAATAGAAGCATTGTGTGCCATCTATATT					
	(157)	157	170	180	190		208
hBRS3	(157)	ACTTATGCTGTGATCATTTTCAGTGGGCATCCTTGAAATGCTATTCTCATCA					
ratBRS3	(157)	ACTTATGCTGTGATCATTTTCAGTGGGCATCCTCGGAAATGCTATCCTCATCA					
rhBRS3	(154)	ACTTATGCTGTGATCATTTTCAGTGGGCATCCTTGAAATGCTATTCTCATCA					
Consensus	(157)	ACTTATGCTGTGATCATTTTCAGTGGGCATCCTTGAAATGCTATTCTCATCA					
	(209)	209	220	230	240	250	260
hBRS3	(209)	AAGTCTTTTTCAAGACCAAATCCATGCAAACAGTTCCAAATATTTTCATCAC					
ratBRS3	(209)	AAGTCTTTTTCAAGACTAAATCCATGCAAACAGTTCCAAATATTTTCATCAC					
rhBRS3	(206)	AAGTCTTTTTCAAGACCAAATCCATGCAAACAGTTCCAAATATTTTCATCAC					
Consensus	(209)	AAGTCTTTTTCAAGACCAAATCCATGCAAACAGTTCCAAATATTTTCATCAC					

FIG.3A

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	(261)	261	270	280	290	300	312
hBRS3	(261)	CAGCCTGGCTTTTGGAGATCTTTACTTCTGCTAACTTGTGTGCCAGTGGAT					
ratBRS3	(261)	CAGCCTGGCTTTTGGAGATCTGTTACTCCTGCTGACTTGTGTGCCAGTGGAT					
rhBRS3	(258)	CAGCCTGGCTTTTGGAGATCTTTACTTCTGCTAACTTGTGTGCCAGTGGAT					
Consensus	(261)	CAGCCTGGCTTTTGGAGATCTTTACTTCTGCTAACTTGTGTGCCAGTGGAT					
	(313)	313	320	330	340	350	364
hBRS3	(313)	GCAACTCACTACCTTGCAGAAGGATGGCTGTTCCGAAGAATTGGTTGTAAGG					
ratBRS3	(313)	GCAACCCACTACCTGGCAGAGGGATGGCTGTTTGGAAGGTCGGTTGTAAAG					
rhBRS3	(310)	GCAACCCACTACCTTGCAGAAGGATGGCTGTTCCGAAGAATTGGTTGTAAGG					
Consensus	(313)	GCAACCCACTACCTTGCAGAAGGATGGCTGTTCCGAAGAATTGGTTGTAAGG					
	(365)	365	370	380	390	400	416
hBRS3	(365)	TGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCAGTGTTCACATTAAC					
ratBRS3	(365)	TGCTTTCCTTCATCCGGCTCACTTCTGTCCGTGTATCAGTGTTCACGCTGAC					
rhBRS3	(362)	TGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCAGTGTTCACGTTAAC					
Consensus	(365)	TGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCAGTGTTCACGTTAAC					
	(417)	417	430	440	450	468	
hBRS3	(417)	AATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAG					
ratBRS3	(417)	AATTCTCAGCGCTGACAGATACAAAGCAGTCGTGAAGCCACTTGAACGACAG					
rhBRS3	(414)	AATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAG					
Consensus	(417)	AATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAG					
	(469)	469	480	490	500	510	520
hBRS3	(469)	CCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCG					
ratBRS3	(469)	CCCTCCAATGCCATTCTGAAGACCTGTGCCAAAGCTGGTGGCATCTGGATCA					
rhBRS3	(466)	CCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCG					
Consensus	(469)	CCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCG					

FIG.3B

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	(521)	521	530	540	550	560	572
hBRS3	(521)	TGCTATGATATTTGCTCTACCTGAGGCTATATTTCAAATGTATACACTTT					
ratBRS3	(521)	TGGCTATGATATTTGCTCTGCCAGAGGCTATATTCTCAAATGTATACACTTT					
rhBRS3	(518)	TGCTATGATATTTGCTCTACCTGAGGCTATATTTCAAATGTATATTCTTT					
Consensus	(521)	TGCTATGATATTTGCTCTACCTGAGGCTATATTTCAAATGTATACACTTT					
	(573)	573	580	590	600	610	624
hBRS3	(573)	TCGAGATCCCAATAAAAAATATGACATTTGAATCATGTACCTCTTATCCTGTC					
ratBRS3	(573)	CCAAGATCCTAACAGAAACGTAACATTTGAATCCTGTAACCTACCCTATC					
rhBRS3	(570)	TCGAGATCCCAACAAAAATGTGACATTTGAATCGTGACCTCTTATCCTGTC					
Consensus	(573)	TCGAGATCCCAACAAAAATGTGACATTTGAATCATGTACCTCTTATCCTGTC					
	(625)	625	630	640	650	660	676
hBRS3	(625)	TCTAAGAAGCTCTTGCAAGAAATACATTCTCTGCTGTGCTTCTTAGTGTCT					
ratBRS3	(625)	TCTGAGAGGCTTTTGCAAGAAATACATTCTCTGTTGTGTTTCTTGGTGTCT					
rhBRS3	(622)	TCTAAGAAGCTCTTGCAAGAAATACATTCTCTGCTGTGCTTCTTAGTGTCT					
Consensus	(625)	TCTAAGAAGCTCTTGCAAGAAATACATTCTCTGCTGTGCTTCTTAGTGTCT					
	(677)	677	690	700	710	728	
hBRS3	(677)	ACATTATCCACTCTCTATTATCTCTGTCTACTATTCCTTGATTGCAGGAC					
ratBRS3	(677)	ACATTATCCCGCTCTCGATTATCTCTGTCTATTATTCTTTGATTGCCAGGAC					
rhBRS3	(674)	ACATTATCCACTCTCTATTATCTCTGTCTATTATTCTTTGATTGCTAGGAC					
Consensus	(677)	ACATTATCCACTCTCTATTATCTCTGTCTATTATTCTTTGATTGCTAGGAC					
	(729)	729	740	750	760	770	780
hBRS3	(729)	CCTTTACAAAAGCACCTGAACATACCTACTGAGGAACAAAGCCATGCCCCGT					
ratBRS3	(729)	TCTTTACAAAAGCACCTGAACATACCGACTGAGGAACAAAGCCATGCCCCGA					
rhBRS3	(726)	CCTTTATAAAAGCACCTGAACATACCTACTGAGGAACAAGGCCATGCCCCGT					
Consensus	(729)	CCTTTACAAAAGCACCTGAACATACCTACTGAGGAACAAAGCCATGCCCCGT					

FIG. 3C

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	(781)	781	790	800	810	820	832
hBRS3	(781)	AAGCAGATTGAATCCCGAAAGAGAATTGCCAGAACGGTATTGGTGTGGTGG					
ratBRS3	(781)	AAGCAGATTGAATCCCGAAAGAGAATTGCCAAAACGGTACTGGTGCTGGTGG					
rhBRS3	(778)	AAGCAGATTGAATCCCGAAAGAGAATTGCCAGAACGGTATTGGTGTGGTGG					
Consensus	(781)	AAGCAGATTGAATCCCGAAAGAGAATTGCCAGAACGGTATTGGTGTGGTGG					

	(833)	833	840	850	860	870	884
hBRS3	(833)	CTCTGTTTGCCCTCTGCTGGTTGCCAAATCACCTCCTGTACCTCTACCATTC					
ratBRS3	(833)	CTCTGTTGCACTCTGCTGGTTGCCGAATCACCTCCTGTATCTCTATCACTC					
rhBRS3	(830)	CTCTGTTTGCCCTCTGCTGGTTGCCAAATCACCTCCTGTACCTCTACCATTC					
Consensus	(833)	CTCTGTTTGCCCTCTGCTGGTTGCCAAATCACCTCCTGTACCTCTACCATTC					

	(885)	885	890	900	910	920	936
hBRS3	(885)	ATTCACCTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTTCATTTTCACC					
ratBRS3	(885)	ATTCACCTTATGAAAGCTACGCAGACCTTCTGATGTCCTTTTCGTTGTCACC					
rhBRS3	(882)	ATTCACCTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTTCATTTTCACC					
Consensus	(885)	ATTCACCTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTTCATTTTCACC					

	(937)	937	950	960	970	988
hBRS3	(937)	ATTTTCTCTCGGGTTTGGCTTTCAGCAATTCTTGCGTAAACCCCTTTGCTC				
ratBRS3	(937)	ATTTTCTCTCGGGTCTGGCTTTCAGTAATCCTGCGTAAACCCCTTTGCTC				
rhBRS3	(934)	ATTTTCTCTCGGGTCTGGCTTTCAGCAATTCTTGCGTAAACCCCTTTGCTC				
Consensus	(937)	ATTTTCTCTCGGGTCTGGCTTTCAGCAATTCTTGCGTAAACCCCTTTGCTC				

	(989)	989	1000	1010	1020	1030	1040
hBRS3	(989)	TCTACTGGCTGAGCAAAACCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTG					
ratBRS3	(989)	TGTATTGGCTGAGCAAGACCTTCCAGAAGCATTTTAAAGGCTCAGCTCTGCTG					
rhBRS3	(986)	TCTACTGGCTGAGCAAAACCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTG					
Consensus	(989)	TCTACTGGCTGAGCAAAACCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTG					

FIG.3D

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	(1041)	1041	1050	1060	1070	1080	1092
hBRS3	(1041)	TTGCAAGGCGGAGCGGCCTGAGCCTCCTGTTGCTGACACCTCTCTTACCACC					
ratBRS3	(1041)	CTTCAAGGCAGAGCAGCCTGAACCTCCTCTTGGTGACACCCCCCTTAACAAC					
rhBRS3	(1038)	TTGCAAGGCAGAGCAGCCTGAGCCTCCTGTTGCTGACACCTCTCTTACCACC					
Consensus	(1041)	TTGCAAGGCAGAGCAGCCTGAGCCTCCTGTTGCTGACACCTCTCTTACCACC					

	(1093)	1093	1100	1110	1120	1130	1144
hBRS3	(1093)	CTGGCTGTGATGGGAACGGTCCCGGGCACTGGGAGCATACAGATGTCTGAAA					
ratBRS3	(1093)	CTCACTGTGATGGGGCGGTTCAGCTACTGGGAGTGACACGTCTCTGAAA					
rhBRS3	(1090)	CTGGCTGTGATGGGAAGGGTCCCGGGCACTGGGAACATGCAGATGTCTGAAA					
	(1093)	CTGGCTGTGATGGGAAGGGTCCCGGGCACTGGGAGCATACAGATGTCTGAAA					

	(1145)	1145	1150	1160	1170	1180	1196
hBRS3	(1145)	TTAGTGTGACCTCGTTCACTGGGTGTAGTGTGAAGCAGGCAGAGACAGATT					
ratBRS3	(1145)	TTAGCGTGACCCTGTTTAGTGGCAGTACTGCCAAGAAAGGAGAGACAAAGT					
rhBRS3	(1142)	TTAGTGTGACCTCGTTCCCTGGGTGTAGTGTGAAGCAGGCAGAGATAGAGT					
Consensus	(1145)	TTAGTGTGACCTCGTTCACTGGGTGTAGTGTGAAGCAGGCAGAGACAGAGT					

	(1197)	1197	2000
hBRS3	(1197)	CTAG	(SEQ. ID NO: 17)
ratBRS3	(1197)	TTAG	(SEQ. ID NO: 18)
rhBRS3	(1194)	CTAG	(SEQ. ID NO: 1)
Consensus	(1197)	CTAG	(SEQ. ID NO: 19)

FIG.3E

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ALIGNMENT OF BRS-3 AMINO ACID SEQUENCES

	(1)	1	10	20	30	40	53
hBRS3	(1)	MAQRQPHSPNQTLISITNDTESSSVVSNNDNTNKGWSDNSPGIEALCAIYIT					
ratBRS3	(1)	MSQRQPQSPNQTLISITNDTETSSSAVSNDTTPKGWTGDNSPGIEALCAIYIT					
rhBRS3	(1)	MAQRQPHSPNQTLISITNDTE-SSSVVSNNDNTNKGWSDNSPGIEALCAIYIT					
Consensus	(1)	MAQRQPHSPNQTLISITNDTESSSVVSNNDNTNKGWSDNSPGIEALCAIYIT					
	(54)	54	60	70	80	90	106
hBRS3	(54)	YAVIISVGILGNAILIKVFFKTKSMQTVPNIFITSLAFGDLLLLLTCVPVDAT					
ratBRS3	(54)	YAVIISVGILGNAILIKVFFKTKSMQTVPNIFITSLAFGDLLLLLTCVPVDAT					
rhBRS3	(53)	YAVIISVGILGNAILIKVFFKTKSMQTVPNIFITSLAFGDLLLLLTCVPVDAT					
Consensus	(54)	YAVIISVGILGNAILIKVFFKTKSMQTVPNIFITSLAFGDLLLLLTCVPVDAT					
	(107)	107	120	130	140		159
hBRS3	(107)	HYLAEGWLFGRIGCKVLSFIRLTSVGVSFVTLTILSADRYKAVVKPLERQPSN					
ratBRS3	(107)	HYLAEGWLFGRIGCKVLSFIRLTSVGVSFVTLTILSADRYKAVVKPLERQPSN					
rhBRS3	(106)	HYLAEGWLFGRIGCKVLSFIRLTSVGVSFVTLTILSADRYKAVVKPLERQPSN					
Consensus	(107)	HYLAEGWLFGRIGCKVLSFIRLTSVGVSFVTLTILSADRYKAVVKPLERQPSN					
	(160)	160	170	180	190	200	212
hBRS3	(160)	AILKTCVKAGCVWIVSMIFALPEAIFSNVYTFRDPNKNMTFESCTSYPVSKKL					
ratBRS3	(160)	AILKTCAGGIWIMAMIFALPEAIFSNVYTFQDPNRNVTFESCNSYPI SERL					
rhBRS3	(159)	AILKTCIKAGCVWIVSMIFALPEAIFSNVYSFRDPNKNVTFESCTSYPVSKKL					
Consensus	(160)	AILKTCIKAGCVWIVSMIFALPEAIFSNVYTFRDPNKNVTFESCTSYPVSKKL					
	(213)	213	220	230	240	250	265
hBRS3	(213)	LQEIHSLLCFLVFYIIPLSIISVYYSLIARTLYKSTLNIPTEEQSHARKQIES					
ratBRS3	(213)	LQEIHSLLCFLVFYIIPLSIISVYYSLIARTLYKSTLNIPTEEQSHARKQIES					
rhBRS3	(212)	LQEIHSLLCFLVFYIIPLSIISVYYSLIARTLYKSTLNIPTEEQSHARKQIES					
Consensus	(213)	LQEIHSLLCFLVFYIIPLSIISVYYSLIARTLYKSTLNIPTEEQSHARKQIES					

FIG. 4A

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	(266)	266	280	290	300	318	
hBRS3	(266)	RKRIARTVLVLVALFALCWLPNHLLYLHSHFTSQTYVDPSAMHFI FTIFSRVL					
ratBRS3	(266)	RKRIAKTVLVLVALFALCWLPNHLLYLHSHFTYESYAEPDVPFVVTIFSRVL					
rhBRS3	(265)	RKRIARTVLVLVALFALCWLPNHLLYLHSHFTSQTYVDPSAMHFI FTIFSRVL					
Consensus	(266)	RKRIARTVLVLVALFALCWLPNHLLYLHSHFTSQTYVDPSAMHFI FTIFSRVL					
<hr/>							
	(319)	319	330	340	350	360	371
hBRS3	(319)	AFSNSCVNPFALYWLKSFQKHFKQLFCCKAERPEPPVADTSLTTLAVMGTV					
ratBRS3	(319)	AFSNSCVNPFALYWLKTFQKHFKQLCCFKAEQPEPPLGDTPLNNLTVMGRV					
rhBRS3	(318)	AFSNSCVNPFALYWLKTFQKHFKQLFCCKAEQPEPPVADTSLTTLAVMGTV					
Consensus	(319)	AFSNSCVNPFALYWLKTFQKHFKQLFCCKAEQPEPPVADTSLTTLAVMGTV					
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	(372)	372	380	399			
hBRS3	(372)	PGTGSIQMSEISVTSFTGCSVKQAEDRF (SEQ. ID NO:20)					
ratBRS3	(372)	PATGSAHVSEISVTLFSGSTAKKGEDKV (SEQ. ID NO:21)					
rhBRS3	(371)	PGTGNMQMSEISVTSFPGCSVKQAEDRV (SEQ. ID NO:2)					
Consensus	(372)	PGTGSIQMSEISVTSFSGCSVKQAEDRV (SEQ. ID NO:22)					

FIG.4B